

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: University College London
- (B) STREET: Rowland Hill Street
- (C) CITY: London
- (D) STATE: none
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): NW3 2PF

(ii) TITLE OF INVENTION: A novel polypeptide hormone phosphatonin

(iii) NUMBER OF SEQUENCES: 25

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTG AAT AAA GAA TAT AGT ATC AGT AAC AAA GAG AAT ACT CAC AAT GGC	48
Val Asn Lys Glu Tyr Ser Ile Ser Asn Lys Glu Asn Thr His Asn Gly	
1 5 10 15	
CTG AGG ATG TCA ATT TAT CCT AAG TCA ACT GGG AAT AAA GGG TTT GAG	96
Leu Arg Met Ser Ile Tyr Pro Lys Ser Thr Gly Asn Lys Gly Phe Glu	
20 25 30	
GAT GGA GAT GAT GCT ATC AGC AAA CTA CAT GAC CAA GAA GAA TAT GGC	144
Asp Gly Asp Asp Ala Ile Ser Lys Leu His Asp Gin Glu Glu Tyr Gly	
35 40 45	
GCA GCT CTC ATC AGA AAT AAC ATG CAA CAT ATA ATG GGG CCA GTG ACT	192
Ala Ala Leu Ile Arg Asn Asn Met Gln His Ile Met Gly Pro Val Thr	
50 55 60	
GCG ATT AAA CTC CTG GGG GAA AAC AAA GAG AAC ACA CCT AGG AAT	240
Ala Ile Lys Leu Leu Gly Glu Gln Asn Lys Glu Asn Thr Pro Arg Asn	
65 70 75 80	

GTT CTA AAC ATA ATC CCA GCA AGT ATG AAT TAT GCT AAA GCA CAC TCG Val Leu Asn Ile Ile Pro Ala Ser Met Asn Tyr Ala Lys Ala His Ser 85 90 95	288
AAG GAT AAA AAG AAG CCT CAA AGA GAT TCC CAA GCC CAG AAA AGT CCA Lys Asp Lys Lys Pro Gln Arg Asp Ser Gln Ala Gln Lys Ser Pro 100 105 110	336
GTA AAA AGC AAA AGC ACC CAT CGT ATT CAA CAC AAC ATT GAC TAC CTA Val Lys Ser Lys Ser Thr His Arg Ile Gln His Asn Ile Asp Tyr Leu 115 120 125	384
AAA CAT CTC TCA AAA GTC AAA AAA ATC CCC AGT GAT TTT GAA GGC AGC Lys His Leu Ser Lys Val Lys Ile Pro Ser Asp Phe Glu Gly Ser 130 135 140	432
GGT TAT ACA GAT CTT CAA GAG AGA GGG GAC AAT GAT ATA TCT CCT TTC Gly Tyr Thr Asp Leu Gln Glu Arg Gly Asp Asn Asp Ile Ser Pro Phe 145 150 155 160	480
AGT GGG GAC GGC CAA CCT TTT AAG GAC ATT CCT GGT AAA GGA GAA GCT Ser Gly Asp Gly Gln Pro Phe Lys Asp Ile Pro Gly Lys Gly Glu Ala 165 170 175	528
ACT GGT CCT GAC CTA GAA GGC AAA GAT ATT CAA ACA GGG TTT GCA GGC Thr Gly Pro Asp Leu Glu Gly Lys Asp Ile Gln Thr Gly Phe Ala Gly 180 185 190	576
CCA AGT GAA GCT GAG AGT ACT CAT CTT GAC ACA AAA AAG CCA GGT TAT Pro Ser Glu Ala Glu Ser Thr His Leu Asp Thr Lys Lys Pro Gly Tyr 195 200 205	624
AAT GAG ATC CCA GAG AGA GAA GAA AAT GGT GGA AAT ACC ATT GGA ACT Asn Glu Ile Pro Glu Arg Glu Glu Asn Gly Gly Asn Thr Ile Gly Thr 210 215 220	672
AGG GAT GAA ACT GCG AAA GAG GCA GAT GCT GTT GAT GTC AGC CTT GTA Arg Asp Glu Thr Ala Lys Glu Ala Asp Ala Val Asp Val Ser Leu Val 225 230 235 240	720
GAG GGC AGC AAC GAT ATC ATG GGT AGT ACC AAT TTT AAG GAG CTC CCT Glu Gly Ser Asn Asp Ile Met Gly Ser Thr Asn Phe Lys Glu Leu Pro 245 250 255	768
GGA AGA GAA GGA AAC AGA GTG GAT GCT GGC AGC CAA AAT GCT CAC CAA Gly Arg Glu Gly Asn Arg Val Asp Ala Gly Ser Gln Asn Ala His Gln 260 265 270	816
GGG AAG GTT GAG TTT CAT TAC CCT CCT GCA CCC TCA AAA GAG AAA AGA Gly Lys Val Glu Phe His Tyr Pro Pro Ala Pro Ser Lys Glu Lys Arg 275 280 285	864
AAA GAA GGC AGT AGT GAT GCA GCT GAA AGT ACC AAC TAT AAT GAA ATT Lys Glu Gly Ser Ser Asp Ala Ala Glu Ser Thr Asn Tyr Asn Glu Ile 290 295 300	912
CCT AAA AAT GGC AAA GGC AGT ACC AGA AAG GGT GTA GAT CAT TCT AAT Pro Lys Asn Gly Lys Gly Ser Thr Arg Lys Gly Val Asp His Ser Asn 305 310 315 320	960

AGG AAC CAA GCA ACC TTA AAT GAA AAA CAA AGG TTT CCT AGT AAG GGC	1008
Arg Asn Gln Ala Thr Leu Asn Glu Lys Gln Arg Phe Pro Ser Lys Gly	
325 330 335	
AAA AGT CAG GGC CTG CCC ATT CCT TCT CGT GGT CTT GAT AAT GAA ATC	1056
Lys Ser Gln Gly Leu Pro Ile Pro Ser Arg Gly Leu Asp Asn Glu Ile	
340 345 350	
AAA AAC GAA ATG GAT TCC TTT AAT GGC CCC AGT CAT GAG AAT ATA ATA	1104
Lys Asn Glu Met Asp Ser Phe Asn Gly Pro Ser His Glu Asn Ile Ile	
355 360 365	
ACA CAT GGC AGA AAA TAT CAT TAT GTA CCC CAC AGA CAA AAT AAT TCT	1152
Thr His Gly Arg Lys Tyr His Tyr Val Pro His Arg Gln Asn Asn Ser	
370 375 380	
ACA CGG AAT AAG GGT ATG CCA CAA GGG AAA GGC TCC TGG GGT AGA CAA	1200
Thr Arg Asn Lys Gly Met Pro Gln Gly Lys Gly Ser Trp Gly Arg Gln	
385 390 395 400	
CCC CAT TCC AAC AGG AGG TTT AGT TCC CGT AGA AGG GAT GAC AGT AGT	1248
Pro His Ser Asn Arg Arg Phe Ser Ser Arg Arg Asp Asp Ser Ser	
405 410 415	
GAG TCA TCT GAC AGT GGC AGT TCA AGT GAG AGC GAT GGT GAC	1290
Glu Ser Ser Asp Ser Gly Ser Ser Glu Ser Asp Gly Asp	
420 425 430	
TAGTCCACCA GGAGTTCCCA GCGGGGTGAC AGTCTGAAGA CCTCGTCACC TGTGAGTTGA	1350
TGTAGAGGAG AGCCACCTGA CAGCTGACCA GGTGAAGAGA GGATAGAGTG AAGAACTGAG	1410
TGAGCCAAGA ATCCTGGTCT CCTTGGGGGA ATTTTGCTA TCTTAATAGT CACAGTATAA	1470
AATTCTATTA AAGGCTATAA TGTTTTAAG CAAAAAAA TCATTACAGA TCTATGAAAT	1530
AGGTAACATT TGAGTAGGTG TCATTTAAAA ATAGTTGGTG AATGTCACAA ATGCCTTCTA	1590
TGTTGTTTGC TCTGTAGACA TGAAAATAAA CAATATCTCT CGATGATAAA AAAAAAAA	1650
AAAAAA	1655

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val Asn Lys Glu Tyr Ser Ile Ser Asn Lys Glu Asn Thr His Asn Gly	
1 5 10 15	
Leu Arg Met Ser Ile Tyr Pro Lys Ser Thr Gly Asn Lys Gly Phe Glu	
20 25 30	

Asp Gly Asp Asp Ala Ile Ser Lys Leu His Asp Gln Glu Glu Tyr Gly
35 40 45

Ala Ala Leu Ile Arg Asn Asn Met Gln His Ile Met Gly Pro Val Thr
50 55 60

Ala Ile Lys Leu Leu Gly Glu Glu Asn Lys Glu Asn Thr Pro Arg Asn
65 70 75 80

Val Leu Asn Ile Ile Pro Ala Ser Met Asn Tyr Ala Lys Ala His Ser
85 90 95

Lys Asp Lys Lys Lys Pro Gln Arg Asp Ser Gln Ala Gln Lys Ser Pro
100 105 110

Val Lys Ser Lys Ser Thr His Arg Ile Gln His Asn Ile Asp Tyr Leu
115 120 125

Lys His Leu Ser Lys Val Lys Lys Ile Pro Ser Asp Phe Glu Gly Ser
130 135 140

Gly Tyr Thr Asp Leu Gln Glu Arg Gly Asp Asn Asp Ile Ser Pro Phe
145 150 155 160

Ser Gly Asp Gly Gln Pro Phe Lys Asp Ile Pro Gly Lys Gly Glu Ala
165 170 175

Thr Gly Pro Asp Leu Gln Gly Lys Asp Ile Gln Thr Gly Phe Ala Gly
180 185 190

Pro Ser Glu Ala Glu Ser Thr His Leu Asp Thr Lys Lys Pro Gly Tyr
195 200 205

Asn Glu Ile Pro Glu Arg Glu Glu Asn Gly Gly Asn Thr Ile Gly Thr
210 215 220

Arg Asp Glu Thr Ala Lys Glu Ala Asp Ala Val Asp Val Ser Leu Val
225 230 235 240

Glu Gly Ser Asn Asp Ile Met Gly Ser Thr Asn Phe Lys Glu Leu Pro
245 250 255

Gly Arg Glu Gly Asn Arg Val Asp Ala Gly Ser Gln Asn Ala His Gln
260 265 270

Gly Lys Val Glu Phe His Tyr Pro Pro Ala Pro Ser Lys Glu Lys Arg
275 280 285

Lys Glu Gly Ser Ser Asp Ala Ala Glu Ser Thr Asn Tyr Asn Glu Ile
290 295 300

Pro Lys Asn Gly Lys Gly Ser Thr Arg Lys Gly Val Asp His Ser Asn
305 310 315 320

Arg Asn Gln Ala Thr Leu Asn Glu Lys Gln Arg Phe Pro Ser Lys Gly
325 330 335

Lys Ser Gln Gly Leu Pro Ile Pro Ser Arg Gly Leu Asp Asn Glu Ile
340 345 350

Lys Asn Glu Met Asp Ser Phe Asn Gly Pro Ser His Glu Asn Ile Ile
355 360 365

Thr His Gly Arg Lys Tyr His Tyr Val Pro His Arg Gin Asn Asn Ser
370 375 380

Thr Arg Asn Lys Gly Met Pro Gln Gly Lys Gly Ser Trp Gly Arg Gln
385 390 395 400

Pro His Ser Asn Arg Arg Phe Ser Ser Arg Arg Arg Asp Asp Ser Ser
405 410 415

Glu Ser Ser Asp Ser Ser Ser Glu Ser Asp Gly Asp
420 425 430

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ser Gly Asp Gly
1

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Asp Ala Val Asp Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ser Ser Arg Arg Arg Asp Asp Ser Ser Glu Ser Ser Asp Ser Gly Ser
1 5 10 15
Ser Ser Glu Ser Asp Gly
20

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ser Ser Arg Ser Lys Glu Asp Ser Asn Ser Thr Glu Ser Lys Ser Ser
1 5 10 15
Ser Glu Glu Asp Gly
20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Asp Ser Ser Glu Ser Ser Asp Ser Gly Ser Ser Ser Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GACGACGACA AGGTGAATAA AGAATATAGT ATCAGTAA

38

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGAACAAAGAC CCGTCTAGTC ACCATCGCTC TCACT

35

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Asp Ser Ser Glu Ser Ser Asp Ser Gly Ser Ser Ser Glu Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Asp Ser Ser Glu Ser Ser Asp Ser Gly Ser Ser Ser Glu Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ser	Ser	Arg	Arg	Arg	Asp	Asp	Ser	Ser	Glu	Ser	Ser	Asp	Ser	Gly	Ser
1				5						10					15
Ser	Ser	Glu	Ser	Asp	Gly										
		20													

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Asp	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Asp	Ser
1				5						10			

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp	Asp	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Asp	Ser
1				5						10			15

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Asp Ser Ser Asp Ser Ser Asp Ser Asn Ser Ser Ser Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ser Ser Glu Ser Ser Asp Ser Ser Asn Ser Ser Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Asp Ser Ser Asp Ser Ser Asp Ser Ser Asn Ser Ser Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ser Asp Glu Ser His His Ser Asp Glu Ser Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Ser Asp Ser Ser Ser Ser Asp Ser Ser Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Ser Asp Ser Ser Asp Ser Ser Asp Ser Ser Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ser Asp Ser Ser Asp Ser Ser Asp Ser Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Ser Ser Arg Ser Lys Glu Asp Ser Asn Ser Thr Glu Ser Lys Ser Ser
1 5 10 15

Ser Glu Glu Asp Gly
20

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGTTATACAG ATCTTCAAGA GAGAG

25

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTTGGTACTT TCAGCTGCAT CACT

24